

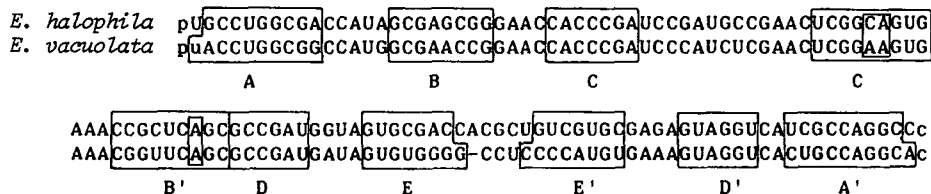
The nucleotide sequences of the 5S rRNAs from the purple bacteria *Ectothiorhodospira halophila* and *Ectothiorhodospira vacuolata*

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5 S rRNA preparations obtained from *Ectothiorhodospira halophila* BN 9624 (strain collection of the department of Microbiology, University of Bonn, FRG) and from *Ectothiorhodospira vacuolata* ATCC 43036 were 3'-terminally labeled by ligation to [5'-<sup>32</sup>P]pCp. Components of different chain length resolved by gel electrophoresis were individually sequenced by the partial chemical degradation method (1). The sequences in the neighbourhood of the 5'-termini were determined by partial nuclease degradation after extension of the 5'-termini by ligation to (Ap)<sub>4</sub>A (2). The following sequences were derived.



Boxes on the alignment enclose double-stranded areas labeled according to a previously documented (3) 5 S RNA secondary structure model. Residues printed in lower case are present in submolar amounts. Three components present in *E. vacuolata* 5 S RNA have the following termini :

pUAC ----- AC (chain length 120)  
 pUAC ----- A (chain length 119)  
 pC ----- A (chain length 118)

The bacteria belonging to the genus *Ectothiorhodospira* were shown (4) by 16 S rRNA oligonucleotide cataloguing to belong to the group of purple bacteria subdivision  $\gamma$  as defined in (5). The same relationship was found (unpublished) when the *Ectothiorhodospira* 5 S RNA sequences were clustered with sequences from 121 bacterial species according to the method described in (6).

#### References

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